



36120C Suppl SL
SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

<130> 28110/36120C

<140> 09/905,743

<141> 2001-07-13

<150> 09/240,639

<151> 1999-01-29

<160> 32

<170> PatentIn version 3.1

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aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga 237
Met Arg
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Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
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Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
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Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
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Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
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act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt 573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
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Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
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cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc 669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
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Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
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ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga 909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
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 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
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gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc 1005
 Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
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tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca 1053
 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
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cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga 1101
 Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
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 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
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 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
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 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
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 Gln Lys Ser Pro Ala Ser

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36120C suppl SL

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35 40 45

Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
50 55 60

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Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
65 70 75 80

Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
85 90 95

Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
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Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
115 120 125

Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
130 135 140

Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
145 150 155 160

Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
165 170 175

Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
180 185 190

Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
195 200 205

Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
210 215 220

Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
225 230 235 240

Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
245 250 255

Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
260 265 270

Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
275 280 285

Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
290 295 300

Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
305 310 315 320

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Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
325 330 335

Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
340 345 350

Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
355 360 365

Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
370 375 380

Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
385 390 395 400

Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
405 410 415

Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
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Met Phe Thr Val Leu Thr Arg Gln Pro Cys

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Ile	Gln	Ile	His	Lys	Gln	Glu	Val	Leu	Pro	Pro	Gly	Leu	Lys	Tyr	Gly	
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Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	Arg	Thr	Thr	Val	Tyr	Val	Tyr	Gln	
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Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asn	Thr	Gly	Val	Val	Ser	Gln	Thr	Phe	
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Lys	Cys	Ser	Val	Lys	Gly	Ser	Gly	Ile	Ser	Ser	Tyr	Gly	Asn	Asn	Pro	
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Gln	Asp	Val	Pro	Arg	Ala	Phe	Glu	Glu	Cys	Met	Gln	Lys	Val	Lys	Gly	
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Gln	Val	Pro	Ser	His	Leu	His	Gly	Ser	Thr	Pro	Ile	His	Leu	Gly	Ala	
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Phe	Arg	Gly	Ala	Gln	Ile	Ile	Ser	Gly	Gln	Glu	Glu	Gly	Val	Tyr	Gly	
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tgg	att	aca	gcc	aac	tat	tta	atg	gga	aat	ttc	ctg	gag	aag	aac	ctg	688
Trp	Ile	Thr	Ala	Asn	Tyr	Leu	Met	Gly	Asn	Phe	Leu	Glu	Lys	Asn	Leu	
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Trp	His	Met	Trp	Val	His	Pro	His	Gly	Val	Glu	Thr	Thr	Gly	Ala	Leu	
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Met	Asp	Leu	Asn	Thr	Ser	Asp	Ile	Met	Gln	Val	Ser	Leu	Tyr	Gly	Tyr	
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ctc Leu	gct Ala	ttc Phe	ttc Phe	aca Thr 495	gtg Val	gca Ala	gcc Ala	ttg Leu	ctg Leu 500	tgt Cys	ctg Leu	gca Ala	ttt Phe	ctt Leu 505	gca Ala	1600

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36120C suppl SL

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Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
35 40 45

Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
50 55 60

Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
65 70 75 80

Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
85 90 95

Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
100 105 110

Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
115 120 125

His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
130 135 140

Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu Val Leu Glu Ser Ile
145 150 155 160

Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
165 170 175

Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
180 185 190

Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp His Met Trp Val His
195 200 205

Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp Leu Gly Gly Ala Ser
210 215 220

Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met Asp Leu Asn Thr Ser
225 230 235 240

Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val Tyr Thr Leu Tyr Thr
245 250 255

His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala Glu Lys Lys Phe Leu
260 265 270

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Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn His Leu Thr Asn Pro
 275 280 285

Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr Met Gly His Val Phe
 290 295 300

Asp Ser Leu Cys Thr Val Asp Gln Arg Pro Glu Ser Tyr Asn Pro Asn
 305 310 315 320

Asp Val Ile Thr Phe Glu Gly Thr Gly Asp Pro Ser Leu Cys Lys Glu
 325 330 335

Lys Val Ala Ser Ile Phe Asp Phe Lys Ala Cys His Asp Gln Glu Thr
 340 345 350

Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys Ile Lys Gly Pro Phe Val
 355 360 365

Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser Ala Leu Asn Leu Ser Gly
 370 375 380

Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser Thr Trp Asn Phe Cys Ser
 385 390 395 400

Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu Pro Lys Phe Asp Glu Val
 405 410 415

Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn Tyr Ile Tyr His Leu Phe
 420 425 430

Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr Trp Pro Gln Ile His Phe
 435 440 445

Glu Lys Glu Val Gly Asn Ser Ser Ile Ala Trp Ser Leu Gly Tyr Met
 450 455 460

Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu Ser Pro Leu Ile Arg Leu
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Pro Ile Glu Pro Pro Val Phe Val Gly Thr Leu Ala Phe Phe Thr Val
 485 490 495

Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala Tyr Leu Cys Ser Ala Thr
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36120C Suppl SL

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	Met	Ala	Thr	Ser	Trp	Gly	Thr	Val	Phe	Phe	Met	Leu	Val	Val	
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Ser	Cys	Val	Cys	Ser	Ala	Val	Ser	His	Arg	Asn	Gln	Gln	Thr	Trp	Phe	
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Glu	Gly	Ile	Phe	Leu	Ser	Ser	Met	Cys	Pro	Ile	Asn	Val	Ser	Ala	Ser	
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gat	caa	cct	aag	cag	ggt	gct	gag	acc	gtt	caa	ggg	ctc	tta	gag	gtg	576
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36120C suppl SL																
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cta Leu	aag Lys	gca Ala	aca Thr 130	gca Ala	gga Gly	cta Leu	cgc Arg	tta Leu 135	ctg Leu	cca Pro	gaa Glu	cac His	aaa Lys 140	gcc Ala	aag Lys	672
gct Ala	ctg Leu	ctc Leu 145	ttt Phe	gag Glu	gta Val	aag Lys	gag Glu 150	atc Ile	ttc Phe	agg Arg	aag Lys	tca Ser 155	cct Pro	ttc Phe	ctg Leu	720
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tta Leu 175	gct Ala	tgg Trp	gtt Val	act Thr	gtg Val 180	aat Asn	ttt Phe	ctg Leu	aca Thr	ggg Gly 185	cag Gln	ctg Leu	cat His	ggc Gly	cac His 190	816
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ctg Leu 255	gga Gly	gcc Ala	ctg Leu	gag Glu	aca Thr 260	gaa Glu	ggg Gly	act Thr	gat Asp	ggg Gly 265	cac His	act Thr	ttc Phe	cgg Arg	agt Ser 270	1056
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tgc Cys	tat Tyr	gcc Ala 305	gaa Glu	gtg Val	ctg Leu	agg Arg	gtg Val 310	gta Val	cga Arg	gga Gly	aaa Lys	ctt Leu 315	cac His	cag Gln	cca Pro	1200
gag Glu	gag Glu 320	gtc Val	cag Gln	aga Arg	ggt Gly	tcc Ser 325	ttc Phe	tat Tyr	gct Ala	ttc Phe	tct Ser 330	tac Tyr	tat Tyr	tat Tyr	gac Asp	1248
cga Arg 335	gct Ala	gtt Val	gac Asp	aca Thr	gac Asp 340	atg Met	att Ile	gat Asp	tat Tyr	gaa Glu 345	aag Lys	ggg Gly	ggt Gly	att Ile	tta Leu 350	1296
aaa Lys	gtt Val	gaa Glu	gat Asp	ttt Phe 355	gaa Glu	aga Arg	aaa Lys	gcc Ala	agg Arg 360	gaa Glu	gtg Val	tgt Cys	gat Asp	aac Asn 365	ttg Leu	1344

36120C suppl SL

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Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385 390 395	
tta cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400 405 410	
ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat	1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415 420 425	
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<213> Homo sapiens

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35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly

65

70

80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320

36120C suppl SL

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
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Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
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aagggagggc ctgaaggacc tccacaggag tgtgagcagc actgcttcag caacaaagcc 180

tcagggtccac atcttgggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231
Met Ala Thr Ser Trp Gly Ala Val Phe
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atg ctg atc ata gcc tgc gtt ggc agc act gtc ttc tac aga gaa cag 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25

36120C Suppl SL

cag Gln	acc Thr	tgg Trp	ttt Phe	gaa Glu 30	ggt Gly	gtc Val	ttc Phe	ttg Leu	tct Ser 35	tcc Ser	atg Met	tgc Cys	ccc Pro	att Ile 40	aat Asn	327
gtc Val	agt Ser	gcc Ala	ggc Gly 45	acc Thr	ttt Phe	tat Tyr	gga Gly 50	att Ile	atg Met	ttt Phe	gat Asp	gcg Ala	ggc Gly 55	agc Ser	act Thr	375
gga Gly	gct Ala	cgg Arg 60	att Ile	cat His	gtt Val	tac Tyr	act Thr 65	ttt Phe	gtg Val	cag Gln	aaa Lys	aca Thr 70	gca Ala	gga Gly	cag Gln	423
ctc Leu	ccc Pro 75	ttt Phe	ctg Leu	gaa Glu	ggt Gly	gaa Glu 80	att Ile	ttt Phe	gat Asp	tct Ser	gtg Val 85	aag Lys	ccg Pro	gga Gly	ctt Leu	471
tct Ser 90	gct Ala	ttt Phe	gtg Val	gat Asp	cag Gln 95	ccc Pro	aaa Lys	cag Gln	ggt Gly	gct Ala 100	gag Glu	act Thr	gtc Val	cag Gln	gag Glu 105	519
ctc Leu	ttg Leu	gag Glu	gtg Val	gcc Ala 110	aaa Lys	gac Asp	tcg Ser	atc Ile	ccc Pro 115	aga Arg	agc Ser	cac His	tgg Trp	gaa Glu 120	agg Arg	567
acc Thr	ccg Pro	gtg Val	gtt Val 125	ctg Leu	aaa Lys	gca Ala	acg Thr	gcc Ala 130	gga Gly	ctc Leu	cgt Arg	ttg Leu	ctg Leu 135	cct Pro	gag Glu	615
cag Gln	aaa Lys	gcc Ala 140	cag Gln	gct Ala	ctg Leu	ctc Leu	ttg Leu 145	gag Glu	gta Val	gag Glu	gag Glu	atc Ile 150	ttc Phe	aag Lys	aat Asn	663
tca Ser	cct Pro 155	ttc Phe	ctg Leu	gtc Val	cca Pro	gat Asp 160	ggc Gly	agc Ser	gtt Val	agc Ser	atc Ile 165	atg Met	gat Asp	ggg Gly	tcc Ser	711
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ctg Leu	cat His	ggt Gly	cgt Arg	ggc Gly 190	cag Gln	gag Glu	act Thr	gtg Val	ggg Gly 195	acc Thr	ctt Leu	gac Asp	ctg Leu	ggg Gly 200	ggt Gly	807
gcc Ala	tcc Ser	acc Thr	caa Gln 205	atc Ile	acg Thr	ttt Phe	cta Leu	ccc Pro 210	cag Gln	ttt Phe	gag Glu	aaa Lys	acc Thr 215	ctg Leu	gaa Glu	855
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aga Arg 250	ctg Leu	gca Ala	act Thr	ctg Leu	gga Gly 255	gcc Ala	ctg Leu	gaa Glu	gca Ala	aaa Lys 260	ggg Gly	act Thr	gat Asp	gga Gly	cat His 265	999
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36120C Suppl SL

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cac cag ctg agg cca agc tcc acc tct gaa gcc tgc att tct gaa cca His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
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ccatcaatgc tgtaattttt tttcttccta cccttattac attccctacc ctaaaagcct	1989
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36120C Suppl SL

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 aaaaaaaaaa 2119

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<212> PRT

<213> Mus musculus

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 20 25 30

Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr
 35 40 45

Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
 50 55 60

Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
 65 70 75 80

Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
 85 90 95

Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
 100 105 110

Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
 115 120 125

Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
 130 135 140

Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
 145 150 155 160

Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
 165 170 175

Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
 180 185 190

36120C Suppl SL

Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
195 200 205

Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
210 215 220

Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
225 230 235 240

Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
245 250 255

Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
260 265 270

Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
290 295 300

Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
305 310 315 320

Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
325 330 335

Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
340 345 350

Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
355 360 365

Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
370 375 380

Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
385 390 395 400

His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
405 410 415

Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
420 425 430

Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val
Page 20

435

440

36120C Suppl SL
445

Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr
 450 455 460

Arg
 465

<210> 9

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<212> PRT

<213> Homo sapiens

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Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160

36120C Suppl SL

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175
 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190
 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220
 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255
 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270
 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285
 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300
 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320
 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335
 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350
 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365
 Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
 370 375 380
 Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
 385 390 395 400
 Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
 405 410 415

36120C Suppl SL

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
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<213> P. sativum

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Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

36120C Suppl SL

Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
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Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val
225 230 235 240

His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu
245 250 255

Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn
260 265 270

Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr
275 280 285

Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu
290 295 300

Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile
305 310 315 320

Trp Asn Gly Gly Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser
325 330 335

Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr
340 345 350

Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu
355 360 365

Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu
370 375 380

Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln
385 390 395 400

Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile
405 410 415

Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala
420 425 430

Trp Pro Leu Gly Asn Ala Val Glu Ala Ile Ser Ala Leu Pro Lys Phe
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435

440

Glu Arg Leu Met Tyr Phe Val
450 455

<210> 11

<211> 454

<212> PRT

<213> Solanum tuberosum

<400> 11

Met Leu Asn Gln Asn Ser His Phe Ile Phe Ile Ile Leu Ala Ile Phe
1 5 10 15

Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile
20 25 30

Pro Leu Arg Arg His Leu Leu Ser His Glu Ser Glu His Tyr Ala Val
35 40 45

Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Phe Arg Phe
50 55 60

Asp Glu Lys Leu Gly Leu Leu Pro Ile Gly Asn Asn Ile Glu Tyr Phe
65 70 75 80

Met Ala Thr Glu Pro Gly Leu Ser Ser Tyr Ala Glu Asp Pro Lys Ala
85 90 95

Ala Ala Asn Ser Leu Glu Pro Leu Leu Asp Gly Ala Glu Gly Val Val
100 105 110

Pro Gln Glu Leu Gln Ser Glu Thr Pro Leu Glu Leu Gly Ala Thr Ala
115 120 125

Gly Leu Arg Met Leu Lys Gly Asp Ala Ala Glu Lys Ile Leu Gln Ala
130 135 140

Val Arg Asn Leu Val Lys Asn Gln Ser Thr Phe His Ser Lys Asp Gln
145 150 155 160

Trp Val Thr Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Met Trp Ala
165 170 175

36120C Suppl SL

Ala Ile Asn Tyr Leu Leu Gly Asn Leu Gly Lys Asp Tyr Lys Ser Thr
 180 185 190

Thr Ala Thr Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala
 195 200 205

Ile Ser Asn Glu Gln Phe Ala Lys Ala Pro Gln Asn Glu Asp Gly Glu
 210 215 220

Pro Tyr Val Gln Gln Lys His Leu Met Ser Lys Asp Tyr Asn Leu Tyr
 225 230 235 240

Val His Ser Tyr Leu Asn Tyr Gly Gln Leu Ala Gly Arg Ala Glu Ile
 245 250 255

Phe Lys Ala Ser Arg Asn Glu Ser Asn Pro Cys Ala Leu Glu Gly Cys
 260 265 270

Asp Gly Tyr Tyr Ser Tyr Gly Gly Val Asp Tyr Lys Val Lys Ala Pro
 275 280 285

Lys Lys Gly Ser Ser Trp Lys Arg Cys Arg Arg Leu Thr Arg His Ala
 290 295 300

Leu Lys Ile Asn Ala Lys Cys Asn Ile Glu Glu Cys Thr Phe Asn Gly
 305 310 315 320

Val Trp Asn Gly Gly Gly Gly Asp Gly Gln Lys Asn Ile His Ala Ser
 325 330 335

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
 340 345 350

Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
 355 360 365

Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
 370 375 380

Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
 385 390 395 400

Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
 405 410 415

Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
 420 425 430

36120C Suppl SL

Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
 435 440 445

Ile Arg Val Ala Ser Ser
 450

<210> 12

<211> 473

<212> PRT

<213> Saccharomyces cerevisiae

<400> 12

Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
 1 5 10 15

Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
 20 25 30

Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
 35 40 45

Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
 50 55 60

Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
 65 70 75 80

Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
 85 90 95

Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
 100 105 110

Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
 115 120 125

Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
 130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly
 145 150 155 160

Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp
 165 170 175

36120C Suppl SL

Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys
180 185 190

Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Gly Ser Thr Gln Ile
195 200 205

Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu
210 215 220

His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln
225 230 235 240

Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn
245 250 255

Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys
260 265 270

Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val
275 280 285

Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr
290 295 300

Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe
305 310 315 320

Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro
325 330 335

Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys
340 345 350

Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr
355 360 365

Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp
370 375 380

Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe
385 390 395 400

Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe
405 410 415

Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp
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420 36120C suppl SL 430
425

Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys
435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
465 470

<210> 13

<211> 153

<212> PRT

<213> Homo sapiens

<400> 13

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
 145 150

<210> 14

<211> 154

<212> PRT

<213> Rattus norvegicus

<400> 14

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
 1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
 35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
 50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
 65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys
 85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
 100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
 115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
 130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
 145 150

<210> 15

<211> 153

<212> PRT

<213> Homo sapiens

36120C Suppl SL

<400> 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16

<211> 150

<212> PRT

<213> Gallus gallus

<400> 16

Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val
1 5 10 15

Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val
20 25 30

36120C Suppl SL

Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr
35 40 45

Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser
50 55 60

Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro
85 90 95

Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr
100 105 110

Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Glu Gly
115 120 125

Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Arg Gly Trp Leu Gly Glu
145 150

<210> 17

<211> 148

<212> PRT

<213> Caenorhabditis elegans

<400> 17

Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu
1 5 10 15

Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp
20 25 30

Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly
35 40 45

Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr
50 55 60

Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly

65

70

80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
130 135 140

Gly Arg Phe Asp
145

<210> 18

<211> 10

<212> RNA

<213> Mus musculus

<400> 18
aagaauagg

10

<210> 19

<211> 10

<212> RNA

<213> Vertebrate

<400> 19
gccgccaugg

10

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20
ccagactgta aatcttttgg

20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21
agggaatgta ataagggtag

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22
ctgcttgagt gacgtctctg

20

<210> 23

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<212> DNA

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<220>

<223> Primer

<400> 23
cacatgaggt tcagctcgtg

20

<210> 24

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<212> DNA

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<400> 24

gtgaagtggc tgccttcagg

20

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

cctttgactc gggactccag

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

gaactgctgc ctaaccactc

20

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27

attgatgggt cttgggattg c

21

<210> 28

<211> 10

<212> RNA

<213> Homo sapiens

<400> 28

augugauga

10

<210> 29

<211> 10

<212> RNA

<213> Homo sapiens

<400> 29

acaaggauga

10

<210> 30

<211> 6

<212> RNA

<213> Homo sapiens

<400> 30

aauaaa

6

<210> 31

<211> 20

<212> DNA

<213> Homo sapiens

<400> 31

caggtcactt atggagcctg

20

<210> 32

36120C Supp1 SL

<211> 18

<212> DNA

<213> Homo sapiens

D10

<400> 32
ccatggacaa aataggac

18